



11

SEQUENCE LISTING

<110> Adams, Sean H
Chui, Clarissa
Goddard, Audrey D
Grimaldi, J. Christopher

<120> BFIT COMPOSITIONS AND METHODS OF USE

<130> 9800081-0066

<140> 10/055,624

<141> 2002-01-22

<150> US 60/263,362

<151> 2002-01-22

<160> 23

<170> PatentIn version 3.2

<210> 1

<211> 1857

<212> DNA

<213> Homo sapiens

<400> 1

gtggaattgc ctttcaa	at gatccaga	at gtcggaa	atc acctgcg	acg gggcttg	gcc	60
tctgtgttct ccaaccg	cac atcccgga	ag tcagcct	tac gtgcggg	gaa cgacagt	gcc	120
atggcagacg gcgaggg	ata ccggaac	ccc acggagg	tgc agatgag	cca gctgggt	gctg	180
ccctgccaca ccaacca	acg tgggtga	gctg agcgtcg	ggc agctgct	caa gtggatt	gac	240
accacggctt gcctgtc	cg ggagagg	cac gctggct	gcc cctgtgt	cac agcttcc	atg	300
gatgacatct attttgag	ca caccatt	agt gttggac	aag tggatga	at caaggcc	aag	360
gtgaaccggg ctttcaac	tc cagcatg	gag gtgggca	tcc aggtggc	ctc ggaggac	ctg	420
tgtcttgaga agcagtgg	aa tgtgtgc	aag gccttgg	cca ctttcgt	ggc ccgccga	gag	480
atcaccaagg tgaagctg	aa gcagatc	acg ccgcgg	acag aagagg	aaa gatggag	cac	540
agtgtggcgg ctgagcg	ccg gcgcat	gcgc cttgtct	atg cagacac	cat caaggac	ctc	600
ctggccaact gcgccatt	ca gggcgat	ctg gagagca	gag actgtag	ccg catgggt	gccg	660
gctgagaaga cccgtgtg	ga gagtgtg	gag ctggtc	cctgc ctcccc	acgc caatcac	cag	720
ggcaacacct ttggggg	cca gatcatg	gcc tggatg	gaga atgtgg	ccac cattgc	agcc	780
agccggctct gccgtgcc	ca ccctacg	tgc aaggcc	attg aaatgt	tcca cttccg	agggc	840
ccgtcccagg tcggcgac	cg tctgggt	gctc aaagcca	tgc tgaaca	atgc cttcaa	acat	900
agcatggagg tgggcgt	gtg cgtggag	gcc tatcgcc	agg aggctg	agac ccaccg	gcgc	960
cacatcaaca gtgccttt	at gaccttt	gtg gtctgg	acg cagatga	cca gccccag	ttg	1020
ctgccctgga ttcggccc	ca gcccggc	gat ggtgag	cggc ggtacc	gaga ggccagt	gcc	1080

agaaagaaga tccgcctgga caggaagtac atcgtgtcct gtaagcagac agaggtgccc 1140
 ctctccgtcc cctgggaccc tagcaaccag gtgtacctga gctacaataa cgtctcctcc 1200
 ttgaagatgc ttgtggccaa ggacaactgg gtgctgtcct cggagatcag tcaggtccgc 1260
 ctgtacactc tggaggatga caagttcctc tccttcaca tggagatggg ggtgcatgtg 1320
 gatgcagccc aggcccttct gctgctctcg gacctgcgc agaggccaga gtgggacaag 1380
 cactaccgga gcgtggagct agtgcagcag gtagacgagg acgacgccat ctaccacgtc 1440
 accagccctg ccctcggagg tcacacaaag cccaggaact tcgtgatcct ggccctcgagg 1500
 cggaagcctt gtgacaatgg ggaccctat gtcacgcgc tgaggtcggg cacgctgccc 1560
 acacaccgag agacgccaga gtacagacgc ggagagaccc tctgctcagg cttctgcctc 1620
 tggcgcgagg gggaccagct gaccaagtgc tgctgggtta gggctctcct gactgagctg 1680
 gtctcggcaa gtggcttcta ttctggggg ctgcaatcca ggtcaaaggg tcgcaggagc 1740
 gacggttgga atggaaaact agctggagga cacctgagta ctcttaaagc aatccccgtg 1800
 gccaaaatca acagccgatt tggatacctt caagacacct gaaaccttat catgagc 1857

<210> 2
 <211> 607
 <212> PRT
 <213> Homo sapiens

<400> 2

Met Ile Gln Asn Val Gly Asn His Leu Arg Arg Gly Leu Ala Ser Val
 1 5 10 15

Phe Ser Asn Arg Thr Ser Arg Lys Ser Ala Leu Arg Ala Gly Asn Asp
 20 25 30

Ser Ala Met Ala Asp Gly Glu Gly Tyr Arg Asn Pro Thr Glu Val Gln
 35 40 45

Met Ser Gln Leu Val Leu Pro Cys His Thr Asn Gln Arg Gly Glu Leu
 50 55 60

Ser Val Gly Gln Leu Leu Lys Trp Ile Asp Thr Thr Ala Cys Leu Ser
 65 70 75 80

Ala Glu Arg His Ala Gly Cys Pro Cys Val Thr Ala Ser Met Asp Asp
 85 90 95

Ile Tyr Phe Glu His Thr Ile Ser Val Gly Gln Val Val Asn Ile Lys
 100 105 110

Ala Lys Val Asn Arg Ala Phe Asn Ser Ser Met Glu Val Gly Ile Gln

115		120		125											
Val	Ala	Ser	Glu	Asp	Leu	Cys	Ser	Glu	Lys	Gln	Trp	Asn	Val	Cys	Lys
130						135					140				
Ala	Leu	Ala	Thr	Phe	Val	Ala	Arg	Arg	Glu	Ile	Thr	Lys	Val	Lys	Leu
145					150					155					160
Lys	Gln	Ile	Thr	Pro	Arg	Thr	Glu	Glu	Glu	Lys	Met	Glu	His	Ser	Val
				165					170					175	
Ala	Ala	Glu	Arg	Arg	Arg	Met	Arg	Leu	Val	Tyr	Ala	Asp	Thr	Ile	Lys
			180					185					190		
Asp	Leu	Leu	Ala	Asn	Cys	Ala	Ile	Gln	Gly	Asp	Leu	Glu	Ser	Arg	Asp
	195						200					205			
Cys	Ser	Arg	Met	Val	Pro	Ala	Glu	Lys	Thr	Arg	Val	Glu	Ser	Val	Glu
	210					215					220				
Leu	Val	Leu	Pro	Pro	His	Ala	Asn	His	Gln	Gly	Asn	Thr	Phe	Gly	Gly
225					230					235					240
Gln	Ile	Met	Ala	Trp	Met	Glu	Asn	Val	Ala	Thr	Ile	Ala	Ala	Ser	Arg
			245						250					255	
Leu	Cys	Arg	Ala	His	Pro	Thr	Leu	Lys	Ala	Ile	Glu	Met	Phe	His	Phe
			260					265					270		
Arg	Gly	Pro	Ser	Gln	Val	Gly	Asp	Arg	Leu	Val	Leu	Lys	Ala	Ile	Val
	275						280					285			
Asn	Asn	Ala	Phe	Lys	His	Ser	Met	Glu	Val	Gly	Val	Cys	Val	Glu	Ala
	290					295					300				
Tyr	Arg	Gln	Glu	Ala	Glu	Thr	His	Arg	Arg	His	Ile	Asn	Ser	Ala	Phe
305					310					315					320
Met	Thr	Phe	Val	Val	Leu	Asp	Ala	Asp	Asp	Gln	Pro	Gln	Leu	Leu	Pro
			325						330					335	
Trp	Ile	Arg	Pro	Gln	Pro	Gly	Asp	Gly	Glu	Arg	Arg	Tyr	Arg	Glu	Ala
			340					345					350		
Ser	Ala	Arg	Lys	Lys	Ile	Arg	Leu	Asp	Arg	Lys	Tyr	Ile	Val	Ser	Cys
	355						360					365			

Lys Gln Thr Glu Val Pro Leu Ser Val Pro Trp Asp Pro Ser Asn Gln
 370 375 380

Val Tyr Leu Ser Tyr Asn Asn Val Ser Ser Leu Lys Met Leu Val Ala
 385 390 395 400

Lys Asp Asn Trp Val Leu Ser Ser Glu Ile Ser Gln Val Arg Leu Tyr
 405 410 415

Thr Leu Glu Asp Asp Lys Phe Leu Ser Phe His Met Glu Met Val Val
 420 425 430

His Val Asp Ala Ala Gln Ala Phe Leu Leu Leu Ser Asp Leu Arg Gln
 435 440 445

Arg Pro Glu Trp Asp Lys His Tyr Arg Ser Val Glu Leu Val Gln Gln
 450 455 460

Val Asp Glu Asp Asp Ala Ile Tyr His Val Thr Ser Pro Ala Leu Gly
 465 470 475 480

Gly His Thr Lys Pro Gln Asp Phe Val Ile Leu Ala Ser Arg Arg Lys
 485 490 495

Pro Cys Asp Asn Gly Asp Pro Tyr Val Ile Ala Leu Arg Ser Val Thr
 500 505 510

Leu Pro Thr His Arg Glu Thr Pro Glu Tyr Arg Arg Gly Glu Thr Leu
 515 520 525

Cys Ser Gly Phe Cys Leu Trp Arg Glu Gly Asp Gln Leu Thr Lys Cys
 530 535 540

Cys Trp Val Arg Val Ser Leu Thr Glu Leu Val Ser Ala Ser Gly Phe
 545 550 555 560

Tyr Ser Trp Gly Leu Glu Ser Arg Ser Lys Gly Arg Arg Ser Asp Gly
 565 570 575

Trp Asn Gly Lys Leu Ala Gly Gly His Leu Ser Thr Leu Lys Ala Ile
 580 585 590

Pro Val Ala Lys Ile Asn Ser Arg Phe Gly Tyr Leu Gln Asp Thr
 595 600 605

<210> 3
 <211> 1818
 <212> DNA

<213> Homo sapiens

<400> 3

gtggaattgc cctttgcatc aaatgatcca gaatgtcggg aatcacctgc gacggggcctt	60
ggcctctgtg ttctccaacc gcacatcccg gaagtcagcc ttacgtgcgg ggaacgacag	120
tgccatggca gacggcgagg gataccggaa cccacggag gtgcagatga gccagctggt	180
gctgccctgc cacaccaacc aacgtggtga gctgagcgtc gggcagctgc tcaagtggat	240
tgacaccacg gcttgccctgt ccgcggagag gcacgctggc tgcccctgtg tcacagcttc	300
catggatgac atctattttg agcacaccat tagtggttga caagtggatga atatcaaggc	360
caaggatgaac cgggccttca actccagcat ggaggtgggc atccaggtgg cctcggagga	420
cctgtgctct gagaagcagt ggaatgtgtg caaggccttg gccaccttcg tggcccgcgg	480
agagatcacc aaggatgaagc tgaagcagat cacgccgcgg acagaagagg agaagatgga	540
gcacagtgtg gcggctgagc gccggcgcat gcgccttgct tatgcagaca ccatcaagga	600
cctcctggcc aactgcgcca ttcaggggca tctggagagc agagactgta gccgcatggt	660
gccggctgag aagaccctgt tggagagtgt ggagctggct ctgcctcccc acgccaatca	720
ccagggaac acctttgggg gccagatcat ggctggatg gagaatgtgg ccaccattgc	780
agccagccgg ctctgccgtg cccaccctac gctgaaggcc attgaaatgt tccacttccg	840
aggcccgctc caggctggcg accgtctggt gctcaaagcc atcgtgaaca atgccttcaa	900
acatagcatg gaggtggggc tgtgcgtgga ggcctatcgc caggaggctg agaccaccg	960
gcgccacatc aacagtgcct ttatgacctt tgtggtcctg gacgcagatg accagcccca	1020
gttctgtccc tggattcggc cccagcccgg cgatggtgag cggcgggtacc gagaggccag	1080
tgccagaaag aagatccgcc tggacaggaa gtacatcgtg tcctgtaagc agacagaggt	1140
gcccctctcc gtcccctggg accctagcaa ccaggtgtac ctgagctaca ataacgtctc	1200
ctccttgaag atgcttgtgg ccaaggacaa ctgggtgctg tcctcggaga tcagtcaggt	1260
ccgcctgtac actctggagg atgacaagtt cctctccttc cacatggaga tgggtggtgca	1320
tgtggatgca gccagggcct tcctgctgct ctcggaacctg cgtcagaggc cagagtggga	1380
caagcactac cggagcgtgg agctagtgcg gcaggtagac gaggacgacg ccatctacca	1440
cgtcaccagc cctgccctcg gaggtcacac aaagccccag gacttcgtga tcctggcctc	1500
gaggcggaag ccttgtgaca atggggaccc ctatgtcatc gcgctgaggt cgggtcacgct	1560
gcccacacac cgagagacgc cagagtacag acgcggagag accctctgct caggcttctg	1620
cctctggcgc gagggggacc agctgaccaa ggtatcctac tacaaccagg ccaccccagg	1680
tgttctcaac tatgtgacca ccaacgtggc cggcctctcc tctgagttct acaccacctt	1740
caaggcttgt gagcagtttc tcttggacaa ccggaatgat ctggcccca gcctccagac	1800

cctctagatg ccctcagc

1818

<210> 4
<211> 594
<212> PRT
<213> Homo sapiens

<400> 4

Met Ile Gln Asn Val Gly Asn His Leu Arg Arg Gly Leu Ala Ser Val
1 5 10 15

Phe Ser Asn Arg Thr Ser Arg Lys Ser Ala Leu Arg Ala Gly Asn Asp
20 25 30

Ser Ala Met Ala Asp Gly Glu Gly Tyr Arg Asn Pro Thr Glu Val Gln
35 40 45

Met Ser Gln Leu Val Leu Pro Cys His Thr Asn Gln Arg Gly Glu Leu
50 55 60

Ser Val Gly Gln Leu Leu Lys Trp Ile Asp Thr Thr Ala Cys Leu Ser
65 70 75 80

Ala Glu Arg His Ala Gly Cys Pro Cys Val Thr Ala Ser Met Asp Asp
85 90 95

Ile Tyr Phe Glu His Thr Ile Ser Val Gly Gln Val Val Asn Ile Lys
100 105 110

Ala Lys Val Asn Arg Ala Phe Asn Ser Ser Met Glu Val Gly Ile Gln
115 120 125

Val Ala Ser Glu Asp Leu Cys Ser Glu Lys Gln Trp Asn Val Cys Lys
130 135 140

Ala Leu Ala Thr Phe Val Ala Arg Arg Glu Ile Thr Lys Val Lys Leu
145 150 155 160

Lys Gln Ile Thr Pro Arg Thr Glu Glu Glu Lys Met Glu His Ser Val
165 170 175

Ala Ala Glu Arg Arg Arg Met Arg Leu Val Tyr Ala Asp Thr Ile Lys
180 185 190

Asp Leu Leu Ala Asn Cys Ala Ile Gln Gly Asp Leu Glu Ser Arg Asp
195 200 205

Cys Ser Arg Met Val Pro Ala Glu Lys Thr Arg Val Glu Ser Val Glu

210	215	220
Leu Val Leu Pro Pro His Ala Asn His Gln Gly Asn Thr Phe Gly Gly		
225	230	235 240
Gln Ile Met Ala Trp Met Glu Asn Val Ala Thr Ile Ala Ala Ser Arg		
	245	250 255
Leu Cys Arg Ala His Pro Thr Leu Lys Ala Ile Glu Met Phe His Phe		
	260	265 270
Arg Gly Pro Ser Gln Val Gly Asp Arg Leu Val Leu Lys Ala Ile Val		
	275	280 285
Asn Asn Ala Phe Lys His Ser Met Glu Val Gly Val Cys Val Glu Ala		
	290	295 300
Tyr Arg Gln Glu Ala Glu Thr His Arg Arg His Ile Asn Ser Ala Phe		
305	310	315 320
Met Thr Phe Val Val Leu Asp Ala Asp Asp Gln Pro Gln Leu Leu Pro		
	325	330 335
Trp Ile Arg Pro Gln Pro Gly Asp Gly Glu Arg Arg Tyr Arg Glu Ala		
	340	345 350
Ser Ala Arg Lys Lys Ile Arg Leu Asp Arg Lys Tyr Ile Val Ser Cys		
	355	360 365
Lys Gln Thr Glu Val Pro Leu Ser Val Pro Trp Asp Pro Ser Asn Gln		
	370	375 380
Val Tyr Leu Ser Tyr Asn Asn Val Ser Ser Leu Lys Met Leu Val Ala		
385	390	395 400
Lys Asp Asn Trp Val Leu Ser Ser Glu Ile Ser Gln Val Arg Leu Tyr		
	405	410 415
Thr Leu Glu Asp Asp Lys Phe Leu Ser Phe His Met Glu Met Val Val		
	420	425 430
His Val Asp Ala Ala Gln Ala Phe Leu Leu Leu Ser Asp Leu Arg Gln		
	435	440 445
Arg Pro Glu Trp Asp Lys His Tyr Arg Ser Val Glu Leu Val Gln Gln		
	450	455 460

Val Asp Glu Asp Asp Ala Ile Tyr His Val Thr Ser Pro Ala Leu Gly
465 470 475 480

Gly His Thr Lys Pro Gln Asp Phe Val Ile Leu Ala Ser Arg Arg Lys
485 490 495

Pro Cys Asp Asn Gly Asp Pro Tyr Val Ile Ala Leu Arg Ser Val Thr
500 505 510

Leu Pro Thr His Arg Glu Thr Pro Glu Tyr Arg Arg Gly Glu Thr Leu
515 520 525

Cys Ser Gly Phe Cys Leu Trp Arg Glu Gly Asp Gln Leu Thr Lys Val
530 535 540

Ser Tyr Tyr Asn Gln Ala Thr Pro Gly Val Leu Asn Tyr Val Thr Thr
545 550 555 560

Asn Val Ala Gly Leu Ser Ser Glu Phe Tyr Thr Thr Phe Lys Ala Cys
565 570 575

Glu Gln Phe Leu Leu Asp Asn Arg Asn Asp Leu Ala Pro Ser Leu Gln
580 585 590

Thr Leu

<210> 5

<211> 2699

<212> DNA

<213> Mus musculus

<400> 5

ctagagatcc	ctcgacctcg	acccacgcgt	ccgagacccc	cccacagcct	ggcaacccag	60
caaacggagc	agcaatgatt	cagaatgtgg	gcaaccactt	gcgaaggggc	ttcgctcta	120
tgttctctaa	tcgcacatcc	cggaagtcaa	tctcccatcc	ggagtctgga	gaccctcta	180
ccatggcaga	gggtgaagga	taccggaacc	ccacggaggt	gcagatgagc	cagctggtac	240
tgccctgcc	acccaaccac	cgtggggagc	tgagcattgg	acagttgctc	aagtggatcg	300
acaccacagc	ctgcctatca	gcggagaggc	atgctggctg	tccttgcgtc	acagcctcta	360
tggatgacat	ctacttcgac	cataccatta	gtgtcggcca	agtggatgaat	atcaaggcca	420
aggtgaaccg	ggccttcaac	tccagcatgg	aggtgggaat	ccaggtgggc	tctgaggatc	480
tgtgctctga	gaagcagtgg	agtgtctgca	aggccttggc	cacctttgtg	gcccaccggg	540
agctctccaa	ggatgaagctg	aagcagggtca	tccattgac	cgaggaggag	aagactgaac	600
atgggggtggc	ggctgagcgc	cggcgtatgc	gactggtcta	tgcagacacc	atcaaagatc	660

tcctaacc	ca	ctgtgtcatc	caggacgatt	tggacaagga	ctgcagcaat	atggtgccag	720
ccgagaagac	ccgagtggag	agtgtggagc	tgggtgctgcc	tcctcacgcc	aatcatcagg		780
gcaatacctt	cgggggacag	atcatggctt	ggatggagaa	tgtggccacc	attgcagcca		840
gccggctctg	tcacgcccac	cctacgctca	aggccatcga	gatgttccat	ttccgaggcc		900
cgtctcaggt	gggggaccgt	ctggtgctca	aggccatcgt	gaataacgcc	tttaagcaca		960
gcatggaggt	gggtgtgtgt	gtggaggcgt	accgccagga	agctgagacc	cagcgccggc		1020
acatcaacag	cgccttcatg	accttcgtgg	tcctggacaa	agatgaccag	cctcagaagc		1080
tgccctggat	tcgtccccag	cctggagagg	gtgaacggcg	ataccgagaa	gccagtgccca		1140
ggaagaagat	ccgcctggac	aggaaatacc	ttgtgtcctg	taagcaggca	gaagtggccc		1200
tgtctgtccc	ctgggaccct	agcaaccagg	tatacctgag	ctactacaac	gtgtcctctc		1260
tgaagacgct	catggccaag	gacaactggg	tgtgtccgt	ggagatcagc	gaggtccgcc		1320
tgtacatcct	agaagaggac	ttcctctcct	ttcacttgga	gatggtggta	aatgtggatg		1380
ccgcccaggt	ctttcagctg	ctgtcagacc	tgcgcaggag	accagagtgg	gacaagcatt		1440
accggagtgt	ggagctgggt	cagcaagtgg	atgaggatga	cgccatctac	cacgtcatca		1500
gccccgccct	gagcgggaac	accaagcccc	aggactttgt	gacctgggcc	tctaggcgga		1560
agccttgtga	caatggggac	ccctatgtca	ttgccctgag	gtcggtcacg	ctgcccacgc		1620
accatgagac	accggaatac	caacgtgggg	agactctctg	ttcaggcttc	tgtctgtggc		1680
gtgaggggga	ccagatgact	aaggtttctt	actacaacca	ggccaccccc	ggctttctca		1740
actatgtgac	caccaatgtg	tccggcctgt	cctcagaatt	ctacaacact	ttcaaggctt		1800
gtgagagttt	tctgttggac	aaccggaatg	acctagctcc	cagcctccag	accctctaga		1860
caccacccat	gctgccccag	gtcttacaca	gtgcgtggaa	caaagcagag	acattttatc		1920
accttgactc	cccaggaag	ccttcacac	tagatggtec	aatcctactg	gatggtcggt		1980
tgtctgtcac	atctgcctgc	aagtctttcc	agtactcctg	ggatatcctg	taatagactc		2040
gggtcctgtc	cacggccctg	gccgcccaca	atccagccca	caaatccaca	tggtgtttcc		2100
cagcagtgtc	gtggtacact	gtgacagtgg	ctctagggga	ggaggccagg	agcctggcca		2160
cagtgttggc	tggactctga	ctcagtggcc	cagcctgcag	ctggaaggac	acaggttgcc		2220
ggagtccctg	acacagctcc	agcatatctg	tgaccatctg	ctcctgataa	ccactgtcca		2280
gcatctcttc	gggccagccc	ggtgccacgg	tcacatgggg	gaagacttca	gccacagctg		2340
tgagcagctc	tctgccagct	atgtggccag	ggaccacaaa	actaccatgt	gagactgtgg		2400
acccaccca	cacaggccag	ggcagatggc	caagggtaga	aaggtgtgct	aacgtggcca		2460
gggatggccg	gagagcttcg	ggttcacta	tgttcacatg	gatgccccag	cgcctgggggt		2520

gaacagccag acgcagcaga cagcactcca gtgtcagagc agggccacct ggggtgtgta 2580
 ggatgggtac aggggttccca gcctcaggtt cctggaggcc aatgtccagc aagatcatgc 2640
 cttctctgtc tggaagaggc aacagtttgg agatcctgtc atcaaaaaaaaa aaaaaaaaaa 2699

<210> 6
 <211> 594
 <212> PRT
 <213> Mus musculus

<400> 6

Met Ile Gln Asn Val Gly Asn His Leu Arg Arg Gly Phe Ala Ser Met
 1 5 10 15

Phe Ser Asn Arg Thr Ser Arg Lys Ser Ile Ser His Pro Glu Ser Gly
 20 25 30

Asp Pro Pro Thr Met Ala Glu Gly Glu Gly Tyr Arg Asn Pro Thr Glu
 35 40 45

Val Gln Met Ser Gln Leu Val Leu Pro Cys His Thr Asn His Arg Gly
 50 55 60

Glu Leu Ser Ile Gly Gln Leu Leu Lys Trp Ile Asp Thr Thr Ala Cys
 65 70 75 80

Leu Ser Ala Glu Arg His Ala Gly Cys Pro Cys Val Thr Ala Ser Met
 85 90 95

Asp Asp Ile Tyr Phe Asp His Thr Ile Ser Val Gly Gln Val Val Asn
 100 105 110

Ile Lys Ala Lys Val Asn Arg Ala Phe Asn Ser Ser Met Glu Val Gly
 115 120 125

Ile Gln Val Val Ser Glu Asp Leu Cys Ser Glu Lys Gln Trp Ser Val
 130 135 140

Cys Lys Ala Leu Ala Thr Phe Val Ala His Arg Glu Leu Ser Lys Val
 145 150 155 160

Lys Leu Lys Gln Val Ile Pro Leu Thr Glu Glu Glu Lys Thr Glu His
 165 170 175

Gly Val Ala Ala Glu Arg Arg Arg Met Arg Leu Val Tyr Ala Asp Thr
 180 185 190

Ile Lys Asp Leu Leu Thr His Cys Val Ile Gln Asp Asp Leu Asp Lys

195	200	205																	
Asp	Cys	Ser	Asn	Met	Val	Pro	Ala	Glu	Lys	Thr	Arg	Val	Glu	Ser	Val				
210						215					220								
Glu	Leu	Val	Leu	Pro	Pro	His	Ala	Asn	His	Gln	Gly	Asn	Thr	Phe	Gly				
225					230					235					240				
Gly	Gln	Ile	Met	Ala	Trp	Met	Glu	Asn	Val	Ala	Thr	Ile	Ala	Ala	Ser				
				245					250					255					
Arg	Leu	Cys	His	Ala	His	Pro	Thr	Leu	Lys	Ala	Ile	Glu	Met	Phe	His				
			260					265					270						
Phe	Arg	Gly	Pro	Ser	Gln	Val	Gly	Asp	Arg	Leu	Val	Leu	Lys	Ala	Ile				
		275					280					285							
Val	Asn	Asn	Ala	Phe	Lys	His	Ser	Met	Glu	Val	Gly	Val	Cys	Val	Glu				
	290					295					300								
Ala	Tyr	Arg	Gln	Glu	Ala	Glu	Thr	Gln	Arg	Arg	His	Ile	Asn	Ser	Ala				
305					310					315					320				
Phe	Met	Thr	Phe	Val	Val	Leu	Asp	Lys	Asp	Asp	Gln	Pro	Gln	Lys	Leu				
				325					330					335					
Pro	Trp	Ile	Arg	Pro	Gln	Pro	Gly	Glu	Gly	Glu	Arg	Arg	Tyr	Arg	Glu				
			340					345					350						
Ala	Ser	Ala	Arg	Lys	Lys	Ile	Arg	Leu	Asp	Arg	Lys	Tyr	Leu	Val	Ser				
		355					360					365							
Cys	Lys	Gln	Ala	Glu	Val	Ala	Leu	Ser	Val	Pro	Trp	Asp	Pro	Ser	Asn				
	370					375					380								
Gln	Val	Tyr	Leu	Ser	Tyr	Tyr	Asn	Val	Ser	Ser	Leu	Lys	Thr	Leu	Met				
385					390					395					400				
Ala	Lys	Asp	Asn	Trp	Val	Leu	Ser	Val	Glu	Ile	Ser	Glu	Val	Arg	Leu				
				405					410					415					
Tyr	Ile	Leu	Glu	Glu	Asp	Phe	Leu	Ser	Phe	His	Leu	Glu	Met	Val	Val				
			420					425					430						
Asn	Val	Asp	Ala	Ala	Gln	Val	Phe	Gln	Leu	Leu	Ser	Asp	Leu	Arg	Arg				
		435					440					445							

Arg Pro Glu Trp Asp Lys His Tyr Arg Ser Val Glu Leu Val Gln Gln
 450 455 460

Val Asp Glu Asp Asp Ala Ile Tyr His Val Ile Ser Pro Ala Leu Ser
 465 470 475 480

Gly Asn Thr Lys Pro Gln Asp Phe Val Ile Leu Ala Ser Arg Arg Lys
 485 490 495

Pro Cys Asp Asn Gly Asp Pro Tyr Val Ile Ala Leu Arg Ser Val Thr
 500 505 510

Leu Pro Thr His His Glu Thr Pro Glu Tyr Gln Arg Gly Glu Thr Leu
 515 520 525

Cys Ser Gly Phe Cys Leu Trp Arg Glu Gly Asp Gln Met Thr Lys Val
 530 535 540

Ser Tyr Tyr Asn Gln Ala Thr Pro Gly Phe Leu Asn Tyr Val Thr Thr
 545 550 555 560

Asn Val Ser Gly Leu Ser Ser Glu Phe Tyr Asn Thr Phe Lys Ala Cys
 565 570 575

Glu Ser Phe Leu Leu Asp Asn Arg Asn Asp Leu Ala Pro Ser Leu Gln
 580 585 590

Thr Leu

<210> 7
 <211> 19
 <212> DNA
 <213> artificial sequence

<220>
 <223> primer oligonucleotide

<400> 7
 tgaaggatac cggaacccc

19

<210> 8
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> probe oligonucleotide

<400> 8
 cggaggtgca gatgagccag ctg

23

<210> 9
 <211> 19
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> primer oligonucleotide

 <400> 9
 tactgccctg ccacaccaa 19

 <210> 10
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> primer oligonucleotide

 <400> 10
 tgctgggtta gggctctcct 20

 <210> 11
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> probe oligonucleotide

 <400> 11
 actgagctgg tctcggaag tggc 24

 <210> 12
 <211> 19
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> primer oligonucleotide

 <400> 12
 tctattcctg ggggctcga 19

 <210> 13
 <211> 21
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> primer oligonucleotide

 <400> 13
 tctcttggac aaccggaatg a 21

 <210> 14
 <211> 20

<212> DNA
 <213> Artificial Sequence

 <220>
 <223> probe oligonucleotide

 <400> 14
 tggccccag cctccagacc 20

<210> 15
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> primer oligonucleotide

 <400> 15
 tctagatgcc ctcaaggcc 20

<210> 16
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> primer oligonucleotide

 <400> 16
 gtaagaagg agcctggag 20

<210> 17
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> primer oligonucleotide

 <400> 17
 tctagaccac cctttctccg 20

<210> 18
 <211> 22
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> primer oligonucleotide

 <400> 18
 ccagaccctc tagatgcct ca 22

<210> 19
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> primer oligonucleotide

 <400> 19
 atgatccaga atgtcggaaa tcac 24

 <210> 20
 <211> 26
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> primer oligonucleotide

 <400> 20
 agacacctga aacottatca tgagcc 26

 <210> 21
 <211> 25
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> primer oligonucleotide

 <400> 21
 gccactgagt cagagtcag ccaac 25

 <210> 22
 <211> 21
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> primer oligonucleotide

 <400> 22
 ccagcctgca gctggaagga c 21

 <210> 23
 <211> 47
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> probe oligonucleotide

 <400> 23
 aaatccacat ggctgttccc agcagtgctg tggtacactg tgacagt 47